IN THE SPECIFICATION

- Please replace the paragraph beginning at page 50, line 1, with the following rewritten paragraph:

-- A second independent PCR amplification of the light chain from cDNA of primate monoclonal antibody 6G5 was effected using a 5' primer early leader sequence of lambda light chain family 2 (primer 745) (SEQ ID NO: 15) and the 3' J region primer 926 (SEQ ID NO: 17). (See Primers for PCR of the lambda light chain variable domain of 6G5 in Tables 1-3 (SEQ ID NOs: 9-25). The isolated PCR product (see technique above) was cloned into TA vector by using the Original TA Cloning(Kit (Invitrogen Catalog # K2000-01). The isolated miniprep DNA (see technique above) was examined under agarose gel electrophoresis after digestion with EcoR I restriction endonuclease. The resultant PCR product comprised in the TA vector was then sequenced (as described previously) using Sp6 (SEQ ID NO: 26) and M13(-40) (SEQ ID NO: 27) forward primers (See Sequencing primers in Table 4 (SEQ ID NOs: 26-35)). The resultant light chain sequence was identical to that of light chain from the first PCR. This entire sequence of the light chain variable domain of primate monoclonal anti-human CD23 antibody 6G5 is presented below (SEQ ID NO: 1) --

- Please replace the captioned paragraph at the bottom of page 50 with the following rewritten paragraph:

-- **Light chain variable region of primate monoclonal antibody anti-human CD23 6G5 Leader**

```
Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr
ATG GCC TGG ACT CTG CTC CTC GTC ACC CTC CTC ACT CAG GGC ACA
                -1
Gly Ser Trp Ala
GGA TCC TGG GCT
```

(SEQ ID NO: 1 – bases 1-57) - -

• Please replace the captioned paragraph beginning at page 51, line 1, with the following rewritten paragraph:

-- **Mature Protein (Numbering is Kabat)**

Framework 1

```
  1                                   9  11
Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser Pro Gly
CAG TCT GCC CCG ACT CAG CCT CCC TCT GTG TCT GGG TCT CCT GGA
                20          23
Gln Ser Val Thr Ile Ser Cys
CAG TCG GTC ACC ATC TCC TGC
```

(SEQ ID NO: 1 – bases 58-123) --

• Please replace the paragraph beginning at page 51, line 9, with the following rewritten paragraph:

-- **CDR 1**

```
 24          27 27A 27B 27C  28                      34
Thr Gly Thr Ser Asp Asp Val Gly Gly Tyr Asn Tyr Val Ser
ACT GGA ACC AGC GAT GAC GTT GGT GGT TAT AAC TAT GTC TCC
```

(SEQ ID NO: 1 – bases 124-165) --

• Please replace the paragraph beginning at page 51, line 13, with the following rewritten paragraph:

-- **Framework 2**

```
 35                  40                                  49
Trp Tyr Gln His His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr
TGG TAC CAA CAC CAC CCA GGC AAA GCC CCC AAA CTC ATG ATT TAT
```

(SEQ ID NO: 1 – bases 166-210) --

- Please replace the paragraph beginning at page 51, line 17, with the following rewritten paragraph:

-- **CDR2**

```
50                                  56

Asp Val Ala Lys Arg Ala Ser

GAT GTC GCT AAG CGG GCC TCA
```

(SEQ ID NO: 1 – bases 211-231) --

- Please replace the paragraph beginning at page 51, line 21, with the following rewritten paragraph:

-- **Framework 3**

```
57          60                                                  70

Gly Val Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala

GGG GTC TCT GAT CGC TTC TCT GGC TCC AAG TCT GGC AAC ACG GCC

                                    80

Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr

TCC CTG ACC ATC TCT GGG CTC CAG GCT GAG GAC GAG GCT GAT TAT

     88

Tyr Cys

TAC TGT
```

(SEQ ID NO: 1 – bases 232-327) --

- Please replace the paragraph beginning at page 52, line 7, with the following rewritten paragraph:

-- **CDR 3**

```
89  90                          95 95A  96  97

Cys Ser Tyr Thr Thr Ser Ser Thr Leu Leu

TGT TCA TAT ACA ACC AGT AGC ACT TTG TTA
```

(SEQ ID NO: 1 – bases 328-357) --

• Please replace the paragraph beginning at page 52, line 11, with the following rewritten paragraph:

-- **Framework 4**

98 100 106 106A 107

Phe Gly Arg Gly Thr Arg Leu Thr Val Leu Gly

TTC GGA AGA GGG ACC CGG TTG ACC GTC CTA GGT (SEQ ID NO: 1 – bases 358-390) --

• Please replace the captioned paragraph beginning at page 52, line 15, with the following rewritten paragraph:

-- 2) **Cloning the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 6G5 by PCR**

The first PCR amplification of the heavy chain variable domain from cDNA of primate monoclonal antibody 6G5 was performer by using the set of early leader sequence primers described supra and the 3' J region primer GE244 (SEQ ID NO: 23). These primers are in Tables 1-3 (SEQ ID NOs: 9-25) infra. This reaction resulted in a 350 base PCR product. This 350 base product (purified as described supra), was digested with Nhe I and Sal I, and ligated into N5LG1 and digested with the same endonucleases in the first PCR amplification. The resultant ligation mixture was transformed into host cells using the same techniques for cloning the light chain. Plasmid N5LG1 containing the 350 base PCR product was then isolated and sequenced (using sequencing primers 266 (SEQ ID NO: 32) and 268) (SEQ ID NO: 33). (These Sequencing primers are set forth in Table 4 (SEQ ID NOs: 26-35).) --

• Please replace the paragraph beginning at page 53, line 10, with the following rewritten paragraph:

-- A second independent PCR reaction was conducted to amplify and isolate the heavy chain variable domain of primate monoclonal antibody 6G5 using a 5' early leader sequence primer for family 1 (MB1503) (SEQ ID NO: 18) and a 3' J' region primer GE244 (SEQ ID NO: 23). (These primers are also contained in Tables 1-3 (SEQ ID NOs: 9-25)) The

resultant PCR product was then cloned into the NSLG1 using the same techniques described supra. Its sequence was found to be identical to the first PCR product. --

- Please replace the paragraph beginning at page 53, line 19, with the following rewritten paragraph:

-- Therefore, in order to clone the whole heavy variable domain of 6G5 including the missing 5' terminus a new longer 3' primer (~~ME1533~~ MB1533) (SEQ ID NO: 25) which included the CDR3 and framework 4 regions of the 6G5 heavy variable chain was then used in a third independent PCR reaction with the family 1 5' primer (MB1503) (SEQ ID NO: 18). (These primers are also contained in Tables 1-3 (SEQ ID NOs: 9-25).) --

- Please replace the paragraph beginning at page 54, line 9, with the following rewritten paragraph:

-- A fourth independent PCR was performed using the same primers as the third PCR amplification. This resulted in a PCR product which was isolated and cloned into the TA vector as described previously. The sequence of the fourth independent PCR product was found to be identical to that obtained in the third PCR amplification. This sequence, which comprises the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 6G5, is presented below (SEQ ID NO: 3). --

- Please replace the captioned paragraph beginning at page 54, line 18, with the following rewritten paragraph:

-- Heavy chain variable region of primate monoclonal antibody anti-human CD23 6G5

Leader

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA
                -1
Trp Val Leu Ser
TGG GTC CTG TCC
```

(SEQ ID NO: 3 – bases 1-57) --

• Please replace the captioned paragraph beginning at page 55, line 1, with the following rewritten paragraph:

-- **Mature Protein (Numbering is Kabat)**

Framework 1

```
1                                                   10
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys Pro Ser
CAG CTG CAG CTG CAG GAG TCG GGC CCA GGA GTG GTG AAG CCT TCG
                20                                          30
Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val Ser
GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCT GTC AGC
```

(SEQ ID NO: 3 – bases 58-147) - -

• Please replace the captioned paragraph beginning at page 55, line 9, with the following rewritten paragraph:

-1 **CDR 1**

```
31                  35 35a
Ser Ser Asn Trp Trp Thr
AGT AGT AAC TGG TGG ACC
```

(SEQ ID NO: 3 – bases 148-165) - -

• Please replace the captioned paragraph beginning at page 55, line 13, with the following rewritten paragraph:

-- **Framework 2**

```
36                  40                                  49
Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
TGG ATC CGC CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT GGA
```

(SEQ ID NO: 3 – bases 166-207) - -

• Please replace the captioned paragraph beginning at page 55, line 17, with the following rewritten paragraph:

-- **CDR2**

```
 50       52 52A  53                                60
Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr Asn Pro Ser Leu
CGT ATC TCT GGT AGT GGT GGG GCC ACC AAC TAC AAC CCG TCC CTC
65
Lys Ser
AAG AGT
```

(SEQ ID NO: 3 – bases 208-258) - -

• Please replace the captioned paragraph beginning at page 56, line 1, with the following rewritten paragraph:

-- **Framework 3**

```
 66                  70                                        80
Arg Val Ile  Ile  Ser Gln Asp Thr Ser Lys Asn Gln Phe Ser Leu
CGA GTC ATC ATT TCA CAA GAC ACG TCC AAG AAC CAG TTC TCC CTG
     82 82a 82b 82c 83                                  90
Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
AAC CTG AAC TCT GTG ACC GCC GCG GAC ACG GCC GTG TAT TAC TGT
     94
Ala Arg
GCC AGA
```

(SEQ ID NO: 3 – bases 259-354) - -

• Please replace the captioned paragraph beginning at page 56, line 11, with the following rewritten paragraph:

-- **CDR 3**

```
 95                  100 100a 100b 100c 100d 101 102
```

Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu Gly Phe

GAT TGG GCC CAA ATA GCT GGA ACA ACG CTA GGC TTC (SEQ ID NO: 3 – bases 355-390) - -

- Please replace the captioned paragraph beginning at page 56, line 15, with the following rewritten paragraph:

Framework 4

103 110 113

Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser

TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA (SEQ ID NO: 3 – bases 391-423)

- -

- Please replace the captioned paragraph beginning at page 57, line 17, with the following rewritten paragraph:

1. Cloning the light chain variable domain of primate monoclonal anti-human CD23 antibody 5E8 by PCR

The first PCR reaction of the light chain variable domain from FEE cDNA was carried out using a set of kappa early leader sequence primers and the 3' J region primer GE204 (SEQ ID NO: 13). (See primers for PCR of the kappa light chain variable domain of 5E8 in Tables 1-3 (SEQ ID NOs: 9-25)). A 420 base PCR product was obtained. The isolated 420 base PCR product was digested with Bgl II and BsiW I restriction endonucleases, cloned into the mammalian expression vector N5KG4P and sequenced using GE108 (SEQ ID NO: 29) and 377 (SEQ ID NO: 30) primers (which are contained in Table 4 (SEQ ID NOs: 26-35)): The mammalian expression vector N5KG4P is identical to the vector N5LG4P except it contains the human kappa light chain constant region is place of the human lambda light chain constant region. Sequencing of this 420 polynucleotide DNA revealed that it contains the entire kappa light chain variable domain. - -

Please replace the paragraph beginning at page 58, line 9, with the following rewritten paragraph:

-- A second independent PCR of the light chain variable region was performed using the 5' family 1 primer GE201 (SEQ ID NO: 9) and the 3' primer GE204 (SEQ ID NO: 13). (See primers for PCR of the kappa light chain variable domain of 5E8 in Tables 1-3 (SEQ ID NOs: 9-25)). The isolated PCR product was cloned into the TA vector (using methods previously described) and sequenced using Sp6 (SEQ ID NO: 26) and T7 promoter (SEQ ID NOs: 28) primers. Sequencing revealed that this PCR product was identical to that obtained from the first PCR. The entire sequence of the light chain variable domain of primate monoclonal anti-human CD23 antibody 5E8 is presented below (SEQ ID NO: 5) --

- Please replace the captioned paragraph beginning at page 59, line 1, with the following rewritten paragraph:

-- **Light chain variable region of primate monoclonal antibody anti-human CD23 5E8**

Leader

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu
ATG GAC ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTT CTG CTC
                          -1
Trp Leu Pro Gly Ala Arg Cys
TGG CTC CCA GGT GCC AGA TGT
```

(SEQ ID NO: 5 – bases 1-66) --

- Please replace the captioned paragraph beginning at page 59, line 9, with the following rewritten paragraph:

-- **Mature Protein (Numbering is Kabat)**

Framework 1

```
1                                   10
```

```
Asp Ile  Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val

GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCT GTA

                  20          23

Gly Asp Arg Val Thr Ile Thr Cys

GGG GAC AGA GTC ACC ATC ACT TGC
```

(SEQ ID NO: 5 – bases 67-135) - -

- Please replace the captioned paragraph beginning at page 59, line 17, with the following rewritten paragraph:

-- **CDR 1**

```
24
                        30                  34
Arg Ala Ser Gln Asp Ile  Arg Tyr Tyr Leu Asn

AGG GCA AGT CAG GAC ATT AGG TAT TAT TTA AAT
```

(SEQ ID NO: 5 – bases 136-168) - -

- Please replace the captioned paragraph beginning at page 59, line 21, with the following rewritten paragraph:

-- **Framework 2**

```
35
                  40                                    49
Try Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  Tyr

TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC TAT
```

(SEQ ID NO: 5 – bases 169-213) - -

- Please replace the captioned paragraph beginning at page 59, line 25, with the following rewritten paragraph:

-- **CDR2**

```
50
                        56
Val Ala Ser Ser Leu Gln Ser
```

GTT GCA TCC AGT TTG CAA AGT (SEQ ID NO: 5 – bases 214-234) - -

• Please replace the captioned paragraph beginning at page 60, line 1, with the following rewritten paragraph:

Framework 3

```
 57          60                                          70
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA GAG TTC
                                    80
Thr Leu Thr Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
ACT CTC ACC GTC AGC AGC CTG CAG CCT GAA GAT TTT GCG ACT TAT
     88
Tyr Cys
TAC TGT (SEQ ID NO: 5 – bases 235-330)
```

• Please replace the captioned paragraph beginning at page 60, line 11, with the following rewritten paragraph:

CDR 3

```
89  90                              97
Leu Gln Val Tyr Ser Thr Pro Arg Thr
CTA CAG GTT TAT AGT ACC CCT CGG ACG (SEQ ID NO: 5 – bases 331-357) - -
```

• Please replace the captioned paragraph beginning at page 60, line 15, with the following rewritten paragraph:

Framework 4

```
98       100                         107
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
```

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA (SEQ ID NO: 5 – bases 358-387) - -

- Please replace the captioned paragraph beginning at page 60, line 19, with the following rewritten paragraph:

- - **2) Cloning the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 5E8 by PCR**

The first PCR of the heavy chain variable domain of 5E8 was performed using a set of 5' early leader heavy chain sequence primers and the 3' primer GE210 (SEQ ID NO: 24). (See primers for PCR of the heavy chain variable domain of 6G5 and 5E8 in Table 1 (SEQ ID NOs: 9-13)). A 420 base PCR product appeared in the family 3 primer reaction. The PCR product was purified and then digested with Nhe I and Sal I and cloned into the mammalian expression vector N5KG4P vector (as described previously). The PCR product was sequenced using the 268 (SEQ ID NO: 33) and 928 (SEQ ID NO: 35) primers. (See sequencing primers in Table 4 (SEQ ID NOs: 26-35).) - -

- Please replace the captioned paragraph beginning at page 61, line 6, with the following rewritten paragraph:

- - A second independent PCR of the heavy chain variable domain of 5E8 was performed using the family 3 5' primer GE207 (SEQ ID NO: 20) and the 3' primer GE210 (SEQ ID NO: 24). (See primers for PCR of the, heavy chain variable domain of 6G5 and 5E8 in Tables 1-3 (SEQ ID NOs: 9-25)). The isolated PCR product was cloned into a TA vector using the same techniques previously described and sequenced by using Sp6 (SEQ ID NO: 26) and T7 (SEQ ID NO: 28) primers. Sequencing revealed that the TAC at codon 91 had been changed into TGC. - -

- Please replace the captioned paragraph beginning at page 61, line 14, with the following rewritten paragraph:

- - In order to determine the appropriate codon at 91, a third independent PCR was performed using the same primers as the second PCR (see above). The PCR product was again cloned into a TA vector and sequenced using Sp6 (SEQ ID NO: 26) and T7 (SEQ ID NO: 28) primers. The sequence was found to be identical to the heavy chain variable

sequence obtained in the first PCR. Therefore, the TGC at position 91 in the second independent PCR product is apparently the result of an error introduced during PCR. This entire sequence of the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 6G5 is presented below (SEQ ID NO: 7).

- Please replace the captioned paragraph beginning at page 62, line 1, with the following rewritten paragraph:

Heavy chain variable region of primate monoclonal antibody anti-human CD23 5E8 Leader

```
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys
ATG GAG TTT GGG CTG AGC TGG GTT TTC CTT GTT CCT CTT TTG AAA
                -1
Gly Val Gln Cys
GGT GTC CAG TGT
```

(SEQ ID NO: 7 - bases 1-57)

- Please replace the captioned paragraph beginning at page 62, line 9, with the following rewritten paragraph:

Mature Protein (Numbering is Kabat)

Framework 1

```
 1                                  10
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys Pro Gly
GAG GTG CAG CTG GTG GAG TCT GGG GGC GGC TTG GCA AAG CCT GGG
                   20                                  30
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe Thr
```

GGG TCC CTG AGA CTC TCC TGC GCA GCC TCC GGG TTC AGG TTC ACC (SEQ ID NO: 7 - bases 58-147) - -

• Please replace the captioned paragraph beginning at page 62, line 17, with the following rewritten paragraph:

- - **CDR 1**

31 35 35a 35b

Phe Asn Asn Tyr Tyr Met Asp

TTC AAT AAC TAC TAC ATG GAC (SEQ ID NO: 7 - bases 148-168)

• Please replace the captioned paragraph beginning at page 62, line 21, with the following rewritten paragraph:

Framework 2

36 40 49

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Ser

TGG GTC CGC CAC GCa CCA GGG CAG GGG CTG GAG TGG GTC TCA (SEQ ID NO: 7 - bases 169-210) - -

• Please replace the captioned paragraph beginning at page 63, line 1, with the following rewritten paragraph:

- - **CDR2**

50 52 52A 53 60

Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp Tyr Ala Asp Ser Val

CGT ATT AGT AGT AGT GGT GAT CCC ACA TGG TAC GCA GAC TCC GTG

65

Lys Gly

AAG GGC (SEQ ID NO: 7 - bases 211-261) - -

• Please replace the captioned paragraph beginning at page 63, line 8, with the following rewritten paragraph:

-- **Framework 3**

```
 66                70                                              80
Arg Phe Thr Ile Ser Arg Glu Asn Ala Asn Asn Thr Leu Phe Leu
AGA TTC ACC ATC TCC AGA GAG AAC GCC AAC AAC ACA CTG TTT CTT
     82 82a 82b 82c 83                              90
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTC TAT TAC TGT
94
Ala Ser
GCG AGC  (SEQ ID NO: 7 - bases 262-357 ) -
```

• Please replace the captioned paragraph beginning at page 63, line 18, with the following rewritten paragraph:

-- **CDR 3**

```
 95                  100 101
Leu Thr Thr Gly Ser Asp Ser
TTG ACT ACA GGG TCT GAC TCC  (SEQ ID NO: 7- bases 358-378) -
```

• Please replace the captioned paragraph beginning at page 63, line 22, with the following rewritten paragraph:

-- **Framework 4**

103 110 113

Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser

TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA (SEQ ID NO: 7 - bases 379-411)

- Please replace the captioned paragraph beginning at page 65, line 3, with the following rewritten paragraph:

A first PCR was done using N5KG4P + 5E8 as a template and a 3' primer (corresponding to codon 71 to 79) and which contains a mutation at codon 75 (AAC changed to AAG, Primer MB1654 (SEQ ID NO: 39), and a 5' primer at the beginning of the leader sequence (Primer MB1650) (SEQ ID NO: 36). (See PCR Primers Used for the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region 5E8 set forth in Table 5 (SEQ ID NOs: 36-39)).

- Please replace the captioned paragraph beginning at page 65, line 10, with the following rewritten paragraph:

A second PCR was performed on the same template by using a 5' primer (corresponding to codon 71 to 79) containing the same mutation (Primer MB1653) (SEQ ID NO: 38) and a 3' primer from the end of framework 4 (Primer MB1651) (SEQ ID NO: 37) (See PCR Primers Used for the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region of 5E8 in Table 5 (SEQ ID NOs: 36-39).)

- Please replace the captioned paragraph beginning at page 65, line 16, with the following rewritten paragraph:

These two PCR products were isolated and mixed in equal molar ratios. A third independent PCR was then carried out by using the mixture of the first and second PCP products as a template with a 5' primer used in the first PCR (MB1650) (SEQ ID NO: 36) and a 3' primer used in the second PCR (MP 1651) (SEQ ID NO: 37) (See PCP Primers Used for the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region in Table 5 (SEQ ID NOs: 36-39).) The PCR product obtained in third PCR was found to contain the heavy variable domain coding region of 5E8 wherein the asparagine 75 had been changed to lysine.

- Please replace Tables 1-5 at page 66, line 12, with the following rewritten Tables 1-5:

Table 1

Primers for PCR of the kappa light chain variable domain of 5E8

NAME	Light chain Vk -early leader 5' (Bgl II)	FAMILY
	-22 -21 -20 -19 -18 -17 -16 -15 -14	
GE201	5' AT CAC AGA TCT CTC ACC ATG GAC ATG AGG GTC CCC GCT CAG 3' (SEQ ID NO: 9)	
GE200	5' AT CAC AGA TCT CTC ACC ATG AGG CTC CCT GCT CAG 3' (SEQ ID NO: 10)	1
GE202	5' AT CAC AGA TCT CTC ACC ATG GAA (A/G)CC CCA GC(T/G) CAG 3' (SEQ ID NO: 11)	2
GE203	5' AT CAC AGA TCT CTC ACC ATG GTG TTG CAG ACC CAG GTC 3' (SEQ ID NO: 12)	3
		4

Light chain Vk-3' primer (BsiW I)

	113 112 111 110 109 108 107 106 105 104 103
GE204	5' GG TGC AGC CAC CGT AGC TTT GAT (C/T)TC CA(G/C) CTT 3' (SEQ ID NO: 13)

Table 2

Primers for PCR of the lambda light chain variable domain of 6G5

NAME **Light chain VI-early leader 5' (Bgl II)** **FAMILY**

-20 -19 -18 -17 -16 -15

744 5' AT CAC AGA TCT CTC ACC ATG (G/A)CC TG(G/C) TCC CCT CT 3' (SEQ ID NO: 14) 1

745 5' AT CAC AGA TCT CTC ACC ATG GCC TGG (A/G)CT C(T/C)G CT 3' (SEQ ID NO: 15) 2

910 5' AT CAC AGA TCT CTC ACC ATG GC(A/C) TGG A(T/C)C CCT CTC 3' (SEQ ID NO: 16) 3

Light chain V1-3' primer (Avr II)

110 109 108 107 106 105 104

926 5' (AC)10 CTT GGG CTG ACC TAG GAC GGT 3' (SEQ ID NO: 17)

Table 3

Primers for PCR of the heavy chain variable domains from 6G5 and 5E8

NAME **Heavy chain-early leaders 5' (Sal I)** **Family**

-20 -19 -18 -17 -16 -15

MB1503 5' GCG ACT AAG TCG ACC ATG GAC TGG ACC TGG 3' (SEQ ID NO: 18) 1

MB1502 5' GCG ACT AAG TCG ACC ATG AAA CAC CTG TGG 3' (SEQ ID NO: 19) 2,4

GE207 5' GCG ACT AAG TCG ACC ATG GAG TTT GGG CTG AGC 3' (SEQ ID NO: 20) 3

GE208 5' GCG ACT AAG TCG ACC ATG GGG TCA ACC GCC ATC 3' (SEQ ID NO: 21) 5

GE209 5' GCG ACT AAG TCG ACC ATG TCT GTC TCC TTC CTC 3' (SEQ ID NO: 22) 6

Heavy chain-3' primer (Nhe I)

120 119 118 117 116 115 114 113 112 111 110

GE244 5' GC CAG GGG GAA GAC CGA TGG GCC CTT GGT GCT AGC TGA GGA GAC GG 3' (SEQ ID NO: 23)

GE210 5' GA TGG GCC CTT GGT GCT AGC TGA GGA GAC GG 3' (SEQ ID NO: 24)

MB1533 5' GGT GCT AGC TGA GGA GAC GGT

109 108 107 106 105 104 103 101 100 99

GAC CAG GAC TCC CTG GCC CCA GAA GCC TAG 3' (SEQ ID NO: 25)

Table 4

Sequencing Primers

Sp6 primer	5' AT TTA GGT GAC ACT ATA 3'	(SEQ ID NO: 26)
M13(-40) Forward Primer	5' GTT TTC CCA GTC ACG A 3'	(SEQ ID NO: 27)
T7 Promoter Primer	5' AT ATA CGA CTC ACT ATA GGG 3'	(SEQ ID NO: 28)
GE 108 Primer	5' CCG TCA GAT CGC CTG GAG ACG CCA 3'	(SEQ ID NO: 29)
377 Primer	5' GCA GTT CCA GAT TTC AAC TG 3'	(SEQ ID NO: 30)
607 PRIMER	5' CCA GGC CAC TGT CAC GGC TTC 3'	(SEQ ID NO: 31)
266 PRIMER	5' CAG AGC TGG GTA CGT CCT CA 3'	(SEQ ID NO: 32)
268 PRIMER	5' GCC CCC AGA GGT GCT CTT GG 3'	(SEQ ID NO: 33)
876 PRIMER	5' ACA CAG ACC CGT CGA CAT GG 3'	(SEQ ID NO: 34)
928 PRIMER	5' GCT CTC GGA GGT GCT CCT GG 3'	(SEQ ID NO: 35)

Table 5

PCR Primers Used for the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region of 5E8

Sal I -20 -19 -18 -17 -16

MB 1650 5' ACA GAC CCG TCG ACC ATG GAG TTT GGG CTG 3' (SEQ ID NO: 36)

Nhe I

118 117 116 115 114 113 112 111 110

MB 1651 5' CCC CTT GGT GCT AGC TGA GGA GAC GGT 3' (SEQ ID NO: 37)

71 72 73 74 75 76 77 78 79
MB 1653 5' AGA GAG AAC GCC AAG AAC ACA CTG TTT 3' (SEQ ID NO: 38)

79 78 77 76 75 74 73 72 71
MB 1654 5' AAA CAG TGT GTT CTT GGC GTT CTC TCT 3' (SEQ ID NO: 39) --